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EXAMINER	
WHISENANT, ETHAN C	
ART UNIT	**PAPER NUMBER**
1634	

DATE MAILED: 03/23/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/882,359	SUBRAMANIAM	
	Examiner	Art Unit	
	Ethan Whisenant, Ph.D.	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *23 December 2003*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-36* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-36* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

FINAL ACTION

1. The applicant's Response (filed 23 DEC 03) to the Office Action has been entered. Following the entry of the paper(s), **Claim(s) 1-36** remain pending. Rejections and/or objections not reiterated from the previous office action are hereby withdrawn. The following rejections and/or objections are either newly applied or reiterated. They constitute the complete set presently being applied to the instant application.

35 USC § 102

2. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that may form the basis for rejections set forth in this Office action:

> A person shall be entitled to a patent unless --
>
> **(a)** the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> **(b)** the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> **(e)** the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.
>
> or
>
> **(e)** the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

3. The changes made to 35 U.S.C. 102(e) by the American Inventors Protection Act of 1999 (AIPA) and the Intellectual Property and High Technology Technical Amendments Act of 2002 do not apply when the reference is a U.S. patent resulting directly or indirectly from an international application filed before November 29, 2000. Therefore, the prior art date of the reference is determined under 35 U.S.C. 102(e) prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. 102(e)).

Claim Rejections under 35 USC § 102

4. **Claim(s) 1-3, 5, 7-11, 13-15, 17, 19-23, 25-27, 29, 31-35** is/are rejected under 35 U.S.C. 102(b) as being anticipated by Stephan et al. (MAY 2000).

Claim 1 is drawn to a method for determining a sequence boundary which method is to comprise four required steps. To begin, a population of addressed fragments of genomic DNA, which fragments are at least 100 nucleotides long, is contacted with a target polynucleotide wherein said target polynucleotide binds a terminal sequence of a DNA region. Next, a relative order for two or more of said addressed fragments is determined. Then, a pair of fragments among said 2 or more addressed fragments that alternatively bind said terminal sequence of a region are identified. Finally, a relative location of a boundary is determined for said sequence of said genomic DNA.

Stephan et al. teach a method for determining a sequence boundary wherein a target polynucleotide (i.e. the NPC1 cDNA) is contacted with a population of genomic DNA fragments which are at least 100 nucleotides long. Note that Stephan et al. teach that their BAC 108N2 fragments following PCR amplification and just before the cloning step are on average 500bp long. Therefore, it is asserted that the fragments that are cloned into the pGEM3Zf+ vector and then subsequently arrayed to form the addressed fragments of genomic DNA are genomic DNA fragments which are at least 100 nucleotides long. See especially the "MATERIALS AND METHODS" section of Stephan et al. Stephan et al. then teach determining a relative order for two or more of said addressed fragments. See Figure 2. Stephan et al. in Figure 2 also teach identifying a pair of fragments among said 2 or more addressed fragments that alternatively bind said terminal sequence of a region. Note, for example, fragment 6 and any of fragments 12, 2, 5, 7, and 8 in Figure 2 panel A. Also note that the legend for Figure 2 on p.14 which teaches that the intron/exon boundaries are identified.

Claim 2 is drawn to an embodiment of the method of Claim **1** wherein said boundary separates an exon from an intron.

As argued above, Stephan et al. teach this limitation wherein these authors teach, for example in the legend for Figure 2 on p.14, that the intron/exon boundaries are identified.

Claim 3 is drawn to an embodiment of the method of Claim 1 wherein said target polynucleotide comprises cDNA.

As argued above, Stephan et al. teach this limitation. See, at least for example, p.12, the last paragraph of the first column.

Claim 5 is drawn to an embodiment of the method of Claim 1 wherein said addressed fragments of eukaryotic genomic DNA are surface bound.

As argued above, Stephan et al. teach this limitation. See, at least for example, p.12 and the section entitled "Preparation of Genomic Array."

Claim 7 is drawn to an embodiment of the method of Claim 5 wherein said surface is a location on an array. As argued above, Stephan et al. teach this limitation. See, at least for example, p.12 and the section entitled "Preparation of Genomic Array." Note also panel A of Figure 2

Claim 8 is drawn to an embodiment of the method of Claim 1 wherein said pair of fragments have a portion of overlapping sequence.

Stephan et al. teach this limitation. See, at least for example, panel A of Figure 2.

Claim 9 is drawn to an embodiment of the method of Claim 1 wherein said pair of fragments have a portion of adjacent sequence compared to said sequence of said genomic DNA

Again, it is asserted that, Stephan et al. teach this limitation. See, at least for example, panel A of Figure 2. Note especially, fragment 6 and any of fragments 12, 2, 5, 7, and 8 in Figure 2 panel A.

Claim 10 is drawn to an embodiment of the method of Claim 1 wherein said addressed fragments of eukaryotic genomic are at least 200 nucleotides length.

As argued above, Stephan et al. teach this limitation. Note that Stephan et al. teach that their BAC 108N2 fragments following PCR amplification and just before the cloning step are on average 500bp long. Therefore, it is asserted that the fragments that are cloned into the pGEM3Zf+ vector and then subsequently arrayed to form the addressed fragments of genomic DNA are genomic DNA fragments which are at least 200 nucleotides long. See especially the "MATERIALS AND METHODS" section of Stephan et al.

Claim 11 is drawn to an embodiment of the method of Claim 1 wherein said addressed fragments of eukaryotic genomic are at least 500 nucleotides length.

As argued above, Stephan et al. teach this limitation. Note that Stephan et al. teach that their BAC 108N2 fragments following PCR amplification and just before the cloning step are on average 500bp long. Therefore, it is asserted that the fragments that are cloned into the pGEM3Zf+ vector and then subsequently arrayed to form the addressed fragments of genomic DNA are genomic DNA fragments which are at least 500 nucleotides long. See especially the "MATERIALS AND METHODS" section of Stephan et al.

Claim 13 is drawn to a method for determining a sequence boundary which method is to comprise four required steps. To begin, a population of surface bound fragments of genomic DNA, which fragments are at least 100 nucleotides long, is contacted with a target polynucleotide wherein said target polynucleotide binds a terminal sequence of a DNA region. Next, a relative order for two or more of said addressed fragments is determined. Then, a pair of fragments among said 2 or more addressed fragments that alternatively bind said terminal sequence of a region are identified. Finally, a relative location of a boundary is determined for said sequence of said genomic DNA.

Stephan et al. teach a method for determining a sequence boundary wherein a target polynucleotide (i.e. the NPC1 cDNA) is contacted with a population of surface bound genomic DNA fragments which are at least 100 nucleotides long. Note that Stephan et al. teach that their BAC 108N2 fragments following PCR amplification and just before the cloning step are on average 500bp long. Therefore, it is asserted that the fragments that are cloned into the pGEM3Zf+ vector and then subsequently arrayed to form the addressed fragments of genomic DNA are genomic DNA fragments which are at least 100 nucleotides long. See especially the "MATERIALS AND METHODS" section of Stephan et al. Stephan et al. then teach determining a relative order for two or more of said addressed fragments. See Figure 2. Stephan et al. in Figure 2 also teach identifying a pair of fragments among said 2 or more surface-bound fragments that alternatively bind said terminal sequence of a region. Note, for example, fragment 6 and any of fragments 12, 2, 5, 7, and 8 in Figure 2 panel A. Also note that the legend for Figure 2 on p.14 which teaches that the intron/exon boundaries are identified.

Claim 14 is drawn to an embodiment of the method of Claim 13 wherein said boundary separates an exon from an intron.

As argued above, Stephan et al. teach this limitation wherein these authors teach, for example in the legend for Figure 2 on p.14, that the intron/exon boundaries are identified.

Claim 15 is drawn to an embodiment of the method of Claim 13 wherein said target polynucleotide comprises cDNA.

As argued above, Stephan et al. teach this limitation. See, at least for example, p.12, the last paragraph of the first column.

Claim 17 is drawn to an embodiment of the method of Claim 13 wherein said addressed fragments of eukaryotic genomic DNA are surface bound.

As argued above, Stephan et al. teach this limitation. See, at least for example, p.12 and the section entitled "Preparation of Genomic Array."

Claim 19 is drawn to an embodiment of the method of Claim 17 wherein said surface is a location on an array. As argued above, Stephan et al. teach this limitation. See, at least for example, p.12 and the section entitled "Preparation of Genomic Array." Note also panel A of Figure 2.

Claim 20 is drawn to an embodiment of the method of Claim 13 wherein said pair of fragments have a portion of overlapping sequence.

Stephan et al. teach this limitation. See, at least for example, panel A of Figure 2.

Claim 21 is drawn to an embodiment of the method of Claim 13 wherein said pair of fragments have a portion of adjacent sequence compared to said sequence of said genomic DNA

Again, it is asserted that, Stephan et al. teach this limitation. See, at least for example, panel A of Figure 2. Note especially, fragment 6 and any of fragments 12, 2, 5, 7, and 8 in Figure 2 panel A.

Claim 22 is drawn to an embodiment of the method of Claim 13 wherein said addressed fragments of eukaryotic genomic are at least 200 nucleotides length.

As argued above, Stephan et al. teach this limitation. Note that Stephan et al. teach that their BAC 108N2 fragments following PCR amplification and just before the cloning step are on average 500bp long. Therefore, it is asserted that the fragments that are cloned into the pGEM3Zf+ vector and then subsequently arrayed to form the addressed fragments of genomic DNA are genomic DNA fragments which are at least 200 nucleotides long. See especially the "MATERIALS AND METHODS" section of Stephan et al.

Claim 23 is drawn to an embodiment of the method of Claim 13 wherein said addressed fragments of eukaryotic genomic are at least 500 nucleotides length.

As argued above, Stephan et al. teach this limitation. Note that Stephan et al. teach that their BAC 108N2 fragments following PCR amplification and just before the cloning step are on average 500bp long. Therefore, it is asserted that the fragments that are cloned into the pGEM3Zf+ vector and then subsequently arrayed to form the addressed fragments of genomic DNA are genomic DNA fragments which are at least 500 nucleotides long. See especially the "MATERIALS AND METHODS" section of Stephan et al.

Claim 25 is drawn to a method for determining a plurality of sequence boundaries which method is to comprise four required steps. To begin, a population of addressed fragments of genomic DNA, which fragments are at least 100 nucleotides long, is contacted with a target polynucleotide wherein said target polynucleotide binds to a plurality of terminal sequences of DNA regions. Next, a relative order for two or more of said addressed fragments is determined for a plurality of sets of 2 or more genomic

DNA fragments. Then, a plurality of pairs of fragments among said plurality of 2 or more addressed fragments that alternatively bind said terminal sequences of regions are identified. Finally, a relative location of boundaries for a plurality of said regions is determined.

Stephan et al. teach a method for determining a plurality of sequence boundaries wherein a target polynucleotide (i.e. the NPC1 cDNA) is contacted with a population of surface bound genomic DNA fragments which are at least 100 nucleotides long. Note that Stephan et al. teach that their BAC 108N2 fragments following PCR amplification and just before the cloning step are on average 500bp long. Therefore, it is asserted that the fragments that are cloned into the pGEM3Zf+ vector and then subsequently arrayed to form the addressed fragments of genomic DNA are genomic DNA fragments which are at least 100 nucleotides long. See especially the "MATERIALS AND METHODS" section of Stephan et al. Stephan et al. then teach determining a relative order for two or more of said addressed fragments for a plurality of sets of 2 or more genomic DNA fragments. See Figure 2. Stephan et al. in Figure 2 also teach identifying a plurality of pairs of fragments among said plurality of 2 or more addressed fragments that alternatively bind said terminal sequences of regions. Note, for example, fragment 6 and any of fragments 12, 2, 5, 7, and 8 in Figure 2 panel A. Also note that the legend for Figure 2 on p.14 which teaches that the intron/exon boundaries are identified. Note also that the relative location of the 3' end of the gene is also determined using the method disclosed by Stephan et al.

Claim 26 is drawn to an embodiment of the method of Claim 25 wherein said boundaries separates exons from intron.

As argued above, Stephan et al. teach this limitation wherein these authors teach, for example in the legend for Figure 2 on p.14, that the intron/exon boundaries are identified.

Claim 27 is drawn to an embodiment of the method of Claim 25 wherein said target polynucleotide comprises cDNA.

As argued above, Stephan et al. teach this limitation. See, at least for example, p.12, the last paragraph of the first column.

Claim 29 is drawn to an embodiment of the method of Claim 25 wherein said addressed fragments of eukaryotic genomic DNA are surface bound.

As argued above, Stephan et al. teach this limitation. See, at least for example, p.12 and the section entitled "Preparation of Genomic Array."

Claim 31 is drawn to an embodiment of the method of Claim 29 wherein said surface is a location on an array.

As argued above, Stephan et al. teach this limitation. See, at least for example, p.12 and the section entitled "Preparation of Genomic Array." Note also panel A of Figure 2.

Claim 32 is drawn to an embodiment of the method of Claim 25 wherein said pairs of fragments have a portions of overlapping sequence.

Stephan et al. teach this limitation. See, at least for example, panel A of Figure 2.

Claim 33 is drawn to an embodiment of the method of Claim 25 wherein said pair of fragments have a portion of adjacent sequence compared to said sequence of said genomic DNA.

Again, it is asserted that, Stephan et al. teach this limitation. See, at least for example, panel A of Figure 2. Note especially, fragment 6 and any of fragments 12, 2, 5, 7, and 8 in panel A of Figure 2.

Claim 34 is drawn to an embodiment of the method of Claim 25 wherein said addressed fragments of eukaryotic genomic DNA are at least 200 nucleotides long.

As argued above, Stephan et al. teach this limitation. Note that Stephan et al. teach that their BAC 108N2 fragments following PCR amplification and just before the cloning step are on average 500bp long. Therefore, it is asserted that the fragments that are cloned into the pGEM3Zf+ vector and then subsequently arrayed to form the addressed fragments of genomic DNA are genomic DNA fragments which are at least 200 nucleotides long. See especially the "MATERIALS AND METHODS" section of Stephan et al.

Claim 35 is drawn to an embodiment of the method of Claim 25 wherein said addressed fragments of eukaryotic genomic are at least 500 nucleotides length.

As argued above, Stephan et al. teach this limitation. Note that Stephan et al. teach that their BAC 108N2 fragments following PCR amplification and just before the cloning step are on average 500bp long. Therefore, it is asserted that the fragments that are cloned into the pGEM3Zf+ vector and then subsequently arrayed to form the addressed fragments of genomic DNA are genomic DNA fragments which are at least 500 nucleotides long. See especially the "MATERIALS AND METHODS" section of Stephan et al.

35 USC § 103

5. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claim Rejections under 35 USC § 103

6. **Claim(s) 4, 16, and 28** is/are rejected under 35 U.S.C. 103(a) as being unpatentable over Stephan et al. (MAY 2000).

Claim 4 is drawn to an embodiment of the method of Claim 1 wherein said target polynucleotide comprises RNA. **Claim 16** is drawn to an embodiment of the method of Claim 13 wherein said target polynucleotide comprises RNA. **Claim 28** is drawn to an embodiment of the method of Claim 25 wherein said target polynucleotide comprises RNA.

Stephan et al. teach a method for determining a sequence boundary or a plurality of sequence boundaries which comprises all of the limitations recited in Claims 4, 16, and 28 except these authors do not explicitly teach using RNA as the target polynucleotide. However, as it is well known in the art that cDNA (i.e. the target polynucleotide used by Stephan et al.) is simply the inverse complement of an mRNA (i.e. an RNA), it would have been, absent an unexpected result, *prima facie* obvious to one of ordinary skill in the art at the time of the invention to use RNA (i.e. NPC1 mRNA) instead of cDNA in the method of Stephan et al. The substitution of one known reagent with known properties for a second well known reagent with known properties is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

7. **Claim(s) 12, 24 and 36** is/are rejected under 35 U.S.C. 103(a) as being unpatentable over Stephan et al. (MAY 2000).

Claim 12 is drawn to an embodiment of the method of Claim 1 wherein said addressed fragments of eukaryotic genomic DNA are at least 1000 nucleotides in length. **Claim 24** is drawn to an embodiment of the method of Claim 13 wherein said addressed fragments of eukaryotic genomic DNA are at least 1000 nucleotides in length. **Claim 36** is drawn to an embodiment of the method of Claim 25 wherein said addressed fragments of eukaryotic genomic DNA are at least 1000 nucleotides in length.

Stephan et al. teach a method for determining a sequence boundary or a plurality of sequence boundaries which comprises all of the limitations recited in Claims 12, 24 and 36 except these authors do not explicitly teach using genomic DNA fragments of at least 1000 bp. Rather, Stephan et al. teach that the arrayed genomic fragments were 500bp average length. However, absent an unexpected result, it would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention that one could with a reasonable expectation of success substitute 1000bp fragments for the 500bp fragments used by Stephan et al. The substitution of one known reagent with known properties for a second well known reagent with known properties is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

8. **Claim(s) 6, 18, 30** is/are rejected under 35 U.S.C. 103(a) as being unpatentable over Stephan et al. (MAY 2000) as applied against Claims 1, 5, 13, 17, 25 and 29 above and further in view of Dale [US 6,562,569 (MAY 03)].

Claim 6 is drawn to an embodiment of the method of Claim 5 wherein said surface is a particle. **Claim 18** is drawn to an embodiment of the method of Claim 17 wherein said surface is a particle. **Claim 30** is drawn to an embodiment of the method of Claim 29 wherein said surface is a particle.

Stephan et al. teach a method for determining a sequence boundary or a plurality of sequence boundaries which comprises all of the limitations recited in Claims 6, 18 and 30 except these authors do not explicitly teach using particles as the surface to address fragments of eukaryotic DNA. Rather, Stephan et al. teach the use of glass slides as the solid support. However, Dale teaches having arrays on beads (i.e. particles) which allows for both the detection of specific nucleic acids and the

isolation of the same nucleic acids. Therefore, absent an unexpected result it would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to modify the method of Stephan et al. wherein beads are used as the solid support instead of glass slides in order to gain the advantages recited by Dale. See Dale Column 22, beginning at about line 45.

RESPONSE TO APPLICANT'S AMENDMENT/ ARGUMENTS

9. Applicant's arguments with respect to the claimed invention have been fully and carefully considered. The applicant has traversed the rejections arguing that "the office action fails to particularly point out each of the elements claimed by in the invention that are allegedly described in Stephan et al. Instead, the office action provides a cursory statement asserting that the cited reference anticipates the claimed invention. Figure 2A is pointed to in the office action as allegedly noting the identification of intron/exon boundaries. Figure 2A a and its associated figure legend refer is a schematic drawing of a CDNA that appears to show its exon structure. Neither the figure or the associated figure legend describe the claimed methods of the invention."

In response the examiner has attempted to address the applicant's concerns by more particularly pointing out the elements present in the Claims that are described in Stephan et al. See the rejections and explanations recited above.

CONCLUSION

10. **Claim(s) 1-36** is/are rejected and/or objected to for the reason(s) set forth above.

11. **THIS ACTION IS MADE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 C.F.R. § 1.136(a).

A SHORTENED STATUTORY PERIOD FOR RESPONSE TO THIS FINAL ACTION IS SET TO EXPIRE THREE MONTHS FROM THE DATE OF THIS ACTION. IN THE EVENT A FIRST RESPONSE IS FILED WITHIN TWO MONTHS OF THE MAILING DATE OF THIS FINAL ACTION AND THE ADVISORY ACTION IS NOT MAILED UNTIL AFTER THE END OF THE THREE-MONTH SHORTENED STATUTORY PERIOD, THEN THE SHORTENED STATUTORY PERIOD WILL EXPIRE ON THE DATE THE ADVISORY ACTION IS MAILED, AND ANY EXTENSION FEE PURSUANT TO 37 C.F.R. § 1.136(a) WILL BE CALCULATED FROM THE MAILING DATE OF THE ADVISORY ACTION. IN NO EVENT WILL THE STATUTORY PERIOD FOR RESPONSE EXPIRE LATER THAN SIX MONTHS FROM THE DATE OF THIS FINAL ACTION.

12. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ethan Whisenant, Ph.D. whose telephone number is (571) 272-0754. The examiner can normally be reached Monday-Friday from 8:30AM -5:30PM EST or any time via voice mail. If repeated attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion, can be reached at (571) 272-0782.

The fax number for this Examiner is (571) 273-0754. Before faxing any papers please inform the examiner to avoid lost papers. Please note that the faxing of papers must conform with the Notice to Comply published in the Official Gazette, 1096 OG 30 (November 15, 1989).

ETHAN WHISENANT
PRIMARY EXAMINER

Art Unit 1634